serological positive.

Conclusion: Analyses of questionnaires showed that leptospirosis had a high prevalence in farmers and herdsmen. So it can be considered as an occupational disease. More occurrence of leptospirosis in male than female is explainable duct a working of more men than women in farms.

doi:10.1016/j.ijid.2010.02.1957

51.026

Epidemiologic comparison of Human *Brucella suis* and *Brucella melitensis* infections

D. Stanek[1,*], P. Nicoletti[2], D. Harrell[3], G. churchwell[4], P. Lee[4], C. Blackmore[5]

[1] *Florida Department of Health, Tallahassee, FL, USA*
[2] *University of Florida College of Veterinary Medicine, Gainesville, FL, USA*
[3] *USDA VS, Gainesville, FL, USA*
[4] *FL DOH, Jacksonville, FL, USA*
[5] *FL DOH, Tallahassee, FL, USA*

Background: Brucella suis is endemic in feral swine across the state of Florida, and with the eradication of *Brucella abortus* in cattle, has emerged as the primary cause of human and animal Brucellosis in the state. *Brucella melitensis* is not present in Florida but is endemic in Mexico. Many Mexican immigrants return to visit friends and family in Mexico regularly, where they may be exposed to *Brucella* through consumption of unpasteurized milk products or domestic animal contact. Although *B. suis* has a worldwide distribution, most epidemiologic case studies describe demographics, clinical presentation and other epidemiologic information from patients infected with *B. melitensis* and *B. abortus*. This study provides an epidemiologic comparison of 36 *B. suis* and 11 *B. melitensis* infected patients reported to Florida Department of Health.

Methods: Human surveillance data from 1997-2008 were reviewed including clinical symptoms and signs, time from symptom onset to treatment and prescribed treatment. Thirty-six patients culture positive for *B. suis* (32 patients), epidemiologically linked to a confirmed patient (1 patient) or serologically confirmed per national guidelines (3 patients) were compared to 11 *B. melitensis* culture positive patients reported during the same timeframe.

Results: Most *B. suis* patients were male (92%), white (94%) and non-Hispanic (81%) with an average age of 43 years (range 18-78). Endocarditis or aneurysm was reported in 4 (11%) of *B suis* patients, two with fatal results. Of the 22 patients with medical treatment information all were prescribed doxycycline, 14 (66%) rifampicin and 13 (62%) an aminoglycoside; 4 (11%) patients relapsed. *Brucella melitensis* patients were 55% male, 55% white and 73% Hispanic. Average age was 37 (range 4-76). Gastrointestinal signs and/or abdominal pain were reported in 4 (36%) of patients, as was single joint or bone pain. Only 4 (44%) of patients were prescribed doxycycline, 2 (22%) rifampicin and 1 (11%) and aminoglycoside; 3 (27%) patients relapsed.

Conclusion: Patient demographics, clinical presentation and clinical management were different for infections with ommendations. Physician education, standardized guidance for convalescent monitoring, and improved testing to reduce incidence of disease relapse are needed.

doi:10.1016/j.ijid.2010.02.1958

Gram-negative Bacterial Infections (Poster Presentation)

52.001

Shigellosis in Central American countries

R. Achí*, K. Barrantes

University of Costa Rica, San José, Costa Rica

Background: Shigellosis is an important cause of morbidity and mortality around the world. *Shigella* spp is transmitted person to person through the faecal-oral route, also by contaminated food and water. The infection is considered as a childhood disease but it also represents an important cause of diarrhea in adults, particularly among tourists who travel to endemic areas. The symptoms range from mild watery diarrhea to severe bacillary dysentery with fever, abdominal pain, blood and mucus in stool samples. The indiscriminate use of antimicrobial drugs is responsible for the increasing resistance among *Shigella* spp. strains worldwide. Even though shigellosis could be a prevalent infection in the region, there are insufficient studies from Central America.

Methods: Fecal specimens from 3045 children up to 10 years old from San José, León, San Salvador and Panama, hospitalized due to severe diarrhea were collected and analyzed at local laboratories using standardized bacterial culture. Samples were inoculated in selective media and analyzed by biochemical tests and serology. Antibiotic susceptibility test was performed to *Shigella* positive strains by the Kirby-Bauer Method (Costa Rica, Nicaragua and El Salvador) and the Biomeriaux Vitek Systems (Panama).

Results: The frequency of *Shigella* in Central American countries was 9.4%(16/170) in Costa Rica, 3.5%(18/508) in Nicaragua, 8.9% (95/1071) in El Salvador and 8.4%(109/1296) in Panama. Eight strains of *S.dysenteriae* (4 from El Salvador y 4 from Panama), 165 of *S.flexneri* (8 from Costa Rica, 14 from Nicaragua, 95 from El Salvador y 109 from Panama), 55 of *S.sonnei* (5 from Costa Rica, 4 from Nicaragua, 20 from El Salvador and 26 from Panama) and 7 of *S. boydii* (El Salvador) were found. Resistance of the *Shigella* isolates to 7 out of 12 antibiotics tested such as Ampicillin, Cephalotin, Gentamicin, Erythromycin, Chloramphenicol, Tetracycline and Trimetroprim-sulfamethoxazole was observed.

Conclusion: Shigella spp is a common pathogen in the Central American region. *S.sonnei* and *S.flexneri* species were the most common agents. In Costa Rica and Nicaragua only *S. flexneri* and *S. sonnei* species were isolated meanwhile in El Salvador and Panama *S. dysenteriae* and El Salvador *S.boydii* were also found. Emergence of resistant-*Shigella* strains to common antibiotics was observed, in particular with Trimethroprim-sulfamethozaxole (more than

60% of strains), Ampiciline, Tetracycline, Erythromycin and Cephalotine.

doi:10.1016/j.ijid.2010.02.1959

52.002

Detection and molecular characterization of verotoxin gene in non-O157 diarrheagenic *Escherichia coli* isolated from Miri hospital, Sarawak, Malaysia

M.N.H. Maziz[1,*], S. ismail[2], H. Jamal[2], A. Ansary[3]

[1] *Universiti Teknologi MARA, Shah Alam, Selangor, Malaysia*
[2] *University of Malaya, Kuala Lumpur, Kuala Lumpur, Malaysia*
[3] *Open University Malaysia, Kuala Lumpur, Malaysia*

Background: Non-O157 diarrheagenic *Escherichia coli* are typical *Escherichia coli*. Infections with non-O157 *Escherichia coli* are now increasingly recognized in many countries. The virulence profiles of most of the non-O157 *E. coli* are unknown. Therefore, easy detection, isolation, and characterization of non-O157 *Escherichia coli* isolates are essential for improving our knowledge of these organisms.

Methods: A total of 32 non-O157 diarrheagenic *Escherichia coli* isolated (Miri hospital, Sarawak, Malaysia, 2001) from the patients with diarrhea were examined for the detection of verotoxin (VT) gene. For this purpose, two sets of primers (VT1 and VT2) were used for PCR method. VT1 probe was prepared which was used for the Southern hybridization study. Bacteriophage induction was carried out using mitomycin C. Nucleotide sequencing was made from the VT1 gene fragment isolated from an *E. coli* isolates using PCR protocol.

Results: The PCR protocol used here produced a fragment of 348 bp of VT1 gene and 584 bp of VT2 gene, respectively. It was shown that 13 *E. coli* isolates (40%) carried VT1 gene whereas none was found to carry VT2 gene using PCR protocols. Plasmids were detected in all the VT1-positive isolates. From the Southern hybridization study, VT1 probe showed homology with the chromosome of all 13 VT1-positive isolates indicating the VT1 gene to be located on chromosome. Bacteriophage induction as carried out using mitomycin C showed that none of the VT1-positive isolates harbor any lysogenic bacteriophage. However, nucleotide sequencing made from the VT1 gene fragment isolated from an *E. coli* isolates using PCR protocol showed 97% homology with the known VT1 gene which proves to be the similar gene carried by *E. coli* O157 and other ancestors.

Conclusion: The PCR method used here was sensitive, specific and reliable. VT1 was found to be the most common verotoxin among the *E. coli* strains isolated from clinical sources in Malaysia and this VT1 gene is located in the chromosome of the *E. coli* isolates. This study improves the knowledge of a highly significant emerging pathogen non-O157 *E. coli*.

doi:10.1016/j.ijid.2010.02.1960

52.003

Isolation and characteristic distribution pattern of *cagA+ Helicobacter pylori* in dental plaque of dyspeptic patients

M. karbalayi[1,*], S. Khodadad[2]

[1] *Tarbiat Modares University, 14113, Iran, Islamic Republic of*
[2] *National Institure of Genetic and Biotechnology research, Tehran, Iran, Islamic Republic of*

Background: Helicobacter pylori is one of the most common human pathogens which colonize in stomach. Recently the oral cavity has been proposed as a reservoir for *H. pylori* but not much evidence from the presence of *cagA*+ H. pylori in dental plaque is available. The aim of this study was to investigate the possibility of isolation of *cagA+ H. pylori* in dental plaque of dyspeptic patients and to study the distribution pattern of *cagA+H. pylori* in different areas of oral cavity.

Methods: One hundred (100) patients with dyspepsia, attending the routine endoscopy were examined and samples from sub gingival plaque of molar and incisor areas of patients were taken, placed in suitable transport media and immediately sent to lab before 4 h. All samples cultured on modified brucella blood agar and all the susceptible colonies were tested by urease, catalase, oxidase and gram stains. Also after DNA extraction process, two sets of primers, highly specific for *ureC* and *cagA* were used for PCR.

Results: H. pylori was detected in dental plaque samples of 40 (40%) of patients by culture on enriched brucella agar media, 100% of these samples were positive by PCR of *ureC* gene and 25 samples (62.5%)were also positive for *cagA* gene. Results of PCR for *ureC* gene on different areas of dental plaque, also showed that sub gingival plaque of molar areas had the most microbial load of *H. pylori* (73%, 29 cases) in comparison of incisor sites (27%, 10 cases).

Conclusion: According to our findings, it's estimated that dental plaque, especially sub gingival plaque of molar areas, can be a suitable reservoir for H. pylori. Being out of reach of oxygen and difficult access of this site for cleaning tools of oral cavity can confirm this thesis. Also it was shown in this study that *cagA + H. pylori* can be isolated from dental plaque of dyspeptic patients, so maybe *H. pylori* can be transmitted by oral route and oral cavity may act as a good source of keeping and re-infecting of stomach of dyspeptic patients after antibiotic therapy

doi:10.1016/j.ijid.2010.02.1961